

20 25 30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
35 40

<210> 32  
<211> 262  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Intron X. Complete length unknown

<400> 32  
gacagtcacc agggggggttg accgcccggac tgggcgtccc cagggttgac tataggacca 60  
gggtgccagg tgccctgcaa gtagaggggc tctcagaggc gtctggotgg catgggtgga 120  
cgtggccccg ggcatggcct tctgcgtgtg ctgcccgtgg tgccctgagc cctcactgag 180  
tcggtggggg cttgtggctt cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240  
cctcctgagg ggctctctat tg 262

<210> 33  
<211> 218  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33  
gtggctgtgc tttggtttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60  
gtatcagctt agatgaaggg cccggaggag gggccacggg acacagccag ggccatggca 120  
cggcgcccac ccatttgtgc gcacagtggg gtggccgagg tgccggtgcc tccagaaaag 180  
cagcgtgggg gtgtaggggg agctcctggg gcaggggac 218

<210> 34  
<211> 2031  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1767)..(1769)  
<223> Wherein N is A, C, G or T

<220>  
<223> Truncated Telomerase

<400> 34  
atgccgcgcg ctccccgctg ccgagccgtg cgtcccttgc tggcgagcca ctaccgcgag 60  
gtgctgcgcg tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120  
cgcggggaac cggcggcctt ccgcgcgctg gtggcccagt gcctggtgtg cgtgcccttg 180  
gacgcacggc cgcgcccccgc cgcgccctcc ttccgccagg tgctctgctt gaaggagctg 240  
gtggcccag tgcgtcacag gctgtgcag cgcggcgaga agaacgtgct ggccttcggc 300  
ttcgogctgc tggacggggc ccgcgggggg ccccccaggg ccttcaccac cagcgtgcgc 360  
agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgct ggggctgctg 420  
ctgcgcgcgc tgggcgacga cgtgctggtt cactgctgg caogctgcgc gctctttgtg 480

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly  
1045 1050 1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe  
1060 1065 1070

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
1075 1080

<210> 51

<211> 2135

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1871)..(1873)

<223> Wherein N is A, C, G or T

<220>

<223> Truncated Telomerase (ver. 2); with  
Intron Y

<400> 51

```
atgccgcgcg ctccccgctg ccgagccgtg cgtccctgc tggcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggcgag 120
cgcgggggacc cggcggtctt ccgcgcgctg gtggcccgag gctgggtgtg cgtgcccgtg 180
gacgcacggc cggccccccg cggccccctc ttccgcccag tgggntccc cggggctggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgccagg 300
gactcagggg gcttcccccg cagggtgctt gcctgaagga gctgggtggc cgagtgtgtc 360
agaggtgtgt cgagcgggc gegaagaacg tgctggcctt cggcttgcg ctgctggacg 420
gggccccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccacaa 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgtgc cgcgtggcg 540
acgaogtgcg ggttcacctg ctggcagcgt gcgcgctctt tgtgctgtgt gctcccagct 600
gcgcctacca ggtgtgcggg ccgcgcgctg accagctcgg cgtgccact caggccccgg 660
ccccgccaca cgctagtggg ccccgaaagg gtctgggatg cgaacggggc tggaaaccata 720
gcgtcaggga ggcgggggtc cccctgggoc tgccagcccc ggggtgcgag aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccaa agaggccccg gcgtggcgct gccccctgag 840
cggagcggac gcccgttggg caggggtcct gggccccacc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctcttgg 960
agggtgcgct ctctggcagc cgcacatccc acccatcgt gggccgcccag caccacgcgg 1020
gccccccate cacatcgagg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcaacttctc tactcctcag gcgacaagga gcagctgcgg ccttctcttc 1140
tactcagctc tctgagggcc agcctgaetg ggcctcggag gctcgtggag accatcttcc 1200
tgggttccag gccctggatg ccagggaact cccgcagggt gccccgcctg ccccgagcgt 1260
actggcaaat gcggccccctg tttctggagc tgcttgggaa ccacgcgcag tgccccctacg 1320
gggtgtcctt caagacgcac tgcccgtgcg gagctgoggt caccacagca gccggtgtct 1380
gtgccccgga gaagccccag ggtctctgtg cggcccccca ggaggaggac acagaccccc 1440
gtgcgctggt gcagctgtct cgcagacaca gcagccccct gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgcgggctg gtgccccag gctctgtggg ctcaggcac aacgaacgcc 1560
gcttctctcag gaacaccaag aagttcatct cctggggaa gcattgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgca gagcaaccgt tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtao gtgctogago tgctcaggtc tttcttttat gtcacggaga 1800
ccacgttcca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaa 1860
gcattggaat nnnagacgtc accagggggg ttgaccgcg gactggcgct cccaggggtt 1920
```

gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggogtctggc 1980  
 tggcatgggt ggacgtggcc ccgggcatgg cettctgcgt gtgctgacgt gggtagccctg 2040  
 agccctcact gagtcgggtg gggcttggg cttcccgta gcttccccc agtctgtgt 2100  
 ctggctgagc aagcctctg aggggctctc tattg 2135

<210> 52  
 <211> 622  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Telomerase (ver.2); encoded  
 by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15  
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
 65 70 75 80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
 85 90 95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser

225                      23                      235                      240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
                                  245                      250                      255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
                                  260                      265                      270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
                                  275                      280                      285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
                                  290                      295                      300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305                                   310                      315                      320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
                                  325                      330                      335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
                                  340                      345                      350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
                                  355                      360                      365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu                      370  
 375                                   380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385                                   390                      395                      400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
                                  405                      410                      415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
                                  420                      425                      430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
                                  435                      440                      445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
                                  450                      455                      460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465                                   470                      475                      480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
                                  485                      490                      495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
                                  500                      505                      510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
                                  515                      520                      525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
                                  530                      535                      540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
610 615 620

<210> 53

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<223> Splicing Variant of Human Telomerase encoded by  
intron Y, ORF2, before the termination codon.  
SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this  
fragment

<400> 53

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala  
65 70 75 80

Ser Gly Trp Gly

<210> 54

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Telomerase (var. 2); encoded  
by SEQ ID NO:51, with Y intron, ORF2, after the  
termination codon

<210> 154  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 154  
 Arg Ala Thr Ser  
 1

<210> 155  
 <211> 622  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Telomerase (ver.2); encoded  
 by SEQ ID NO:51, with Y Intron ORF3

<400> 155  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15  
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
 65 70 75 80  
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
 85 90 95  
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

176